WEST Search History

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DATE: Tuesday, December 07, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L28	L27 not l25	42
☐	L27	l5 and L26	46
☐	L26	Miller-J$.in. or Pabo-C$.in.	8086
☐	L25	l5 and L24	6
☐	L24	Joung-J$.in.	97
	DB=USPT; PLUR=YES; OP=OR		
☐	L23	US-6300488-B1.did.	1
☐	L22	US-6493433-B2.did.	1
☐	L21	US-6300488-B1.did.	1
☐	L20	US-6493433-B2.did.	1
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L19	L10 and l17	8
☐	L18	dimer$ with (activat$ and (requir$ or necess$ or need$))	810
☐	L17	dimer$ with (activat$ and (requir$ or necess$ or need$)) with transcription	61
☐	L16	L10 and L15	40
☐	L15	(test or library) with (dimer$ and (peptide or polypeptide or protein))	774
☐	L14	l12 and L13	1
☐	L13	dimer$ with (requir$ or necess$ or need$) with transcription	101
☐	L12	l10 and L11	40
☐	L11	(test or library) with dimer$	1626
☐	L10	l7 or l8	170
☐	L9	L8 not l7	61
☐	L8	(((DNA adj bind$ adj domain) or DBD) with activat$) same (fusion and dimer$)	139
☐	L7	(((DNA adj bind$ adj domain) or DBD) with fusion) same (activat$ and dimer$)	109
☐	L6	((DNA adj bind$ adj domain) with fusion) same activat$	1721
☐	L5	((DNA adj bind$ adj domain) (w) fusion) same activat$	73059
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L4	lac$ and l1	1
☐	L3	activat$ adj domain and l1	1

☐	L2	activat$ and L1	1
☐	L1	20020119498.pn.	1

END OF SEARCH HISTORY

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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	SEP 01	INPADOC: New family current-awareness alert (SDI) available
NEWS	4	SEP 01	New pricing for the Save Answers for SciFinder Wizard within STN Express with Discover!
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NEWS	6	SEP 27	STANDARDS will no longer be available on STN
NEWS	7	SEP 27	SWETSCAN will no longer be available on STN
NEWS	8	OCT 28	KOREAPAT now available on STN
NEWS	9	NOV 18	Current-awareness alerts, saved answer sets, and current search transcripts to be affected by CERAB, COMPUAB, ELCOM, and SOLIDSTATE reloads
NEWS	10	NOV 30	PHAR reloaded with additional data
NEWS	11	DEC 01	LISA now available on STN

NEWS EXPRESS	OCTOBER 29 CURRENT WINDOWS VERSION IS V7.01A, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
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FILE 'HOME' ENTERED AT 21:26:03 ON 07 DEC 2004

=> fil medline biosis caplus embase wpids

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
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FILE 'MEDLINE' ENTERED AT 21:26:29 ON 07 DEC 2004

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FILE 'WPIDS' ENTERED AT 21:26:29 ON 07 DEC 2004
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=> DNA(w)Binding(w)Domain
L1 26309 DNA(W) BINDING(W) DOMAIN

=> activation(w)domain
L2 9597 ACTIVATION(W) DOMAIN

=> dimer?
L3 360756 DIMER?

=> l1 and l2 and l3
L4 297 L1 AND L2 AND L3

=> test or library
L5 2912493 TEST OR LIBRARY

=> l4 and l5
L6 36 L4 AND L5

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 25 DUP REM L6 (11 DUPLICATES REMOVED)

=> t ti l7 1-25

L7 ANSWER 1 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Novel compound comprising two portions obtained from steroids, hormones or drugs, joined by enzyme cleavable moiety such as amide or cephem moiety, useful for screening proteins capable of catalyzing bond cleavage.

L7 ANSWER 2 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI Bacterial small-mol. three-hybrid system comprising **dimeric** Mtx-SLF ligand that bridges λcI and NTD fusion proteins for detecting protein-small molecule interactions

L7 ANSWER 3 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New non-single chain antigen-binding units stabilized by leucine zipper sequences, useful for diagnostic and therapeutic purposes, and as building blocks for constructing multivalent and/or multispecific antibodies.

L7 ANSWER 4 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Expression and influence of Jun factors in erythroid and megakaryocytic differentiation of primary human hematopoietic progenitors.

L7 ANSWER 5 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Synthetic derivatives of DNA-binding peptides for use in the therapeutic regulation of gene expression

L7 ANSWER 6 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Yeast three-hybrid system for in vivo drug screening and enzyme evolution

using chemical inducers of **dimerization**

L7 ANSWER 7 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New covalent chemical inducers used in high throughput screening of complementary DNA libraries.

L7 ANSWER 8 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Covalent chemical inducer of protein **dimerization**, useful for **dimerizing** two fusion proteins inside a cell, comprises substrates capable of selectively binding to receptors.

L7 ANSWER 9 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Improved reverse n-hybrid screening method for peptides inhibiting protein-protein or nucleic acid-protein interaction

L7 ANSWER 10 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Inducing cell to generate detectable signal and detecting entity within cell, comprises allowing stable interaction of first reporter and second reporter by binding with the entity and generating signal.

L7 ANSWER 11 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New chemical inducer of **dimerization** useful in methods of screening.

L7 ANSWER 12 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Novel chimeric protein useful for modulating exogenous gene expression in subjects, comprises two functional protein units, each containing **dimerization** domain of steroid/thyroid hormone nuclear receptor superfamily.

L7 ANSWER 13 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Detection of peptide modulators of protein-protein biological interactions using a transformed cellular three-hybrid system

L7 ANSWER 14 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Histone deacetylase inhibitors for activating hormone-responsive genes.

L7 ANSWER 15 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New method of screening for modulators of viral matrix protein interaction, useful for treating acute respiratory disease.

L7 ANSWER 16 OF 25 MEDLINE on STN DUPLICATE 2
TI Identification of protein-protein interactions of the major sperm protein (MSP) of Caenorhabditis elegans.

L7 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Using genetic means to dissect homologous and heterologous protein-protein interactions of PKR, the interferon-induced protein kinase

L7 ANSWER 18 OF 25 MEDLINE on STN
TI hMAF, a small human transcription factor that heterodimerizes specifically with Nrf1 and Nrf2.

L7 ANSWER 19 OF 25 MEDLINE on STN
TI A novel, transformation-relevant **activation domain** in Fos proteins.

L7 ANSWER 20 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 3
TI Interactions between Drosophila USP and ECR-A was identified in yeast two-hybrid system.

L7 ANSWER 21 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Modified cells for testing cpds. for peptide binding activity - express two fusion proteins, each containing one member of a binding pair and one domain of a transcriptional activation protein, and also a reporter gene associated with this protein.

L7 ANSWER 22 OF 25 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI Isolation of NF-E2-related factor 2 (Nrf2), a NF-E2-like basic leucine zipper transcriptional activator that binds to the tandem NF-E2/AP1 repeat of the β-globin locus control region.

L7 ANSWER 23 OF 25 MEDLINE on STN DUPLICATE 4
TI Interactions among vertebrate helix-loop-helix proteins in yeast using the two-hybrid system.

L7 ANSWER 24 OF 25 MEDLINE on STN DUPLICATE 5
TI Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Jun.

L7 ANSWER 25 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI THE TWO-HYBRID SYSTEM A METHOD TO IDENTIFY AND CLONE GENES FOR PROTEINS THAT INTERACT WITH A PROTEIN OF INTEREST.

=> d ibib abs l7 2,6,7,13,20-25

L7 ANSWER 2 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2003:855546 CAPLUS
DOCUMENT NUMBER: 139:346749
TITLE: Bacterial small-mol. three-hybrid system comprising **dimeric** Mtx-SLF ligand that bridges λcI and NTD fusion proteins for detecting protein-small molecule interactions
INVENTOR(S): Althoff, Eric A.; Cornish, Virginia W.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 28 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003203471	A1	20031030	US 2002-132039	20020424
WO 2004042345	A2	20040521	WO 2003-US12612	20030424
WO 2004042345	A3	20040923		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-132039 A2 20020424
OTHER SOURCE(S): MARPAT 139:346749
AB The present invention provides a transgenic bacterial cell comprising (a)

a **dimeric** small mol. which comprises a first moiety known to bind a first receptor domain covalently linked to a second moiety known to bind a second receptor domain; (b) nucleotide sequences which upon transcription encode (i) a first fusion protein comprising the first receptor domain, and (ii) a second fusion protein comprising the second receptor domain; and (c) a reporter gene wherein expression of the reporter gene is conditioned on the proximity of the first fusion protein to the second fusion protein. The cell is also adapted for use in a method for identifying a mol. that binds to a known target in a bacterial cell from a pool of candidate mols., and a method for identifying an unknown target receptor to which a mol. is capable of binding in a bacterial cell. Also described are compds. and kits for carrying out the methods. The examples describe the synthetic preparation of a heterodimer of methotrexate and a synthetic analog of FK507 (SLF), referred to as Mtx-SLF. Mtx-SLF was used to **dimerize** a λcI-FK506 binding protein 12 protein chimera and an αNTD-dihydrofolate reductase protein chimera.

L7 ANSWER 6 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:31914 CAPLUS
DOCUMENT NUMBER: 136:98820
TITLE: Yeast three-hybrid system for in vivo drug screening and enzyme evolution using chemical inducers of **dimerization**
INVENTOR(S): Cornish, Virginia W.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 48 pp., Cont.-in-part of U.S. Ser. No. 490,320.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002004202	A1	20020110	US 2001-768479	20010124
US 2004106154	A1	20040603	US 2003-705644	20031110
PRIORITY APPLN. INFO.:			US 2000-490320 A2	20000124
			US 2001-768479 A3	20010124

AB The disclosed invention relates to the evolution of enzymes in vivo, and drug screening in vivo through the use of chemical inducers of protein **dimerization**. The subject invention provides a compound having the formula: H1--X--B-Y--H2 wherein each of H1 and H2 may be the same or different and capable of binding to a receptor which is the same or different; wherein each of X and Y may be present or absent and if present, each may be the same or different spacer moiety; and wherein B is an enzyme cleavable moiety. This invention also provides a method of screening proteins for the ability to catalyze bond cleavage or bond formation, comprising the steps of: (a) providing a cell that expresses a pair of fusion proteins which upon **dimerization** change a cellular readout; (b) providing the compound of the invention which **dimerizes** the pair of fusion proteins, said compound comprising two portions coupled by a bond that is cleavable or formed by the protein to be screened; and (c) screening for the cellular readout, wherein a change the cellular readout indicates catalysis of bond cleavage or bond formation by the protein to be screened. However, it has not heretofore been suggested to use small mol. induced protein **dimerization** to screen for catalysis in vivo., and specifically, it has not been suggested to use an enzyme cleavable moiety to link two mols. to **dimerize** proteins. This invention provides proteins de novo with prescribed binding and catalytic properties and permits screening cDNA libraries

based on biochem. function. Practically, we believe that powerful screens in combination with existing randomization techniques will make it possible to take an existing protein fold and evolve it into an enzyme with a new function generating useful catalysts for the pharmaceutical and chemical industries. Since the screen is done in vivo and in both prokaryotes and eukaryotes, the methodol. can be applied to functional genomics and drug discovery. A new chemical inducer of **dimerization** (CID) was recently developed in Professor Cornish's lab, which uses a heterodimer of methotrexate (MTX) and dexamethasone (DEX) which, when placed in the yeast three-hybrid system, reconstitutes transcription of the lacZ gene. The effects of altering the structure of the DEX-MTX CID and the protein chimeras in the three-hybrid assay were investigated. It was observed that all DEX-MTX CIDs, except the DEX-MTX CID with the shortest chemical linker, showed the ability to induce β-galactosidase levels at levels 400% above strains possessing no CID. The DEX-MTX CIDs showed little or no increase in β-galactosidase levels above background levels in strains where dihydrofolate reductase (DHFR) from E. coli was replaced by DHFR from murine. The three-hybrid system did show some directional preference to the way in which the receptors where fused to the **DNA binding domain** and the **activation domain**. These studies have led to a better understanding of the factors that are important in activating transcription in the DEX-MTX yeast three-hybrid system.

L7 ANSWER 7 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-627419 [67] WPIDS
CROSS REFERENCE: 2003-361751 [34]
DOC. NO. CPI: C2004-012699
TITLE: New covalent chemical inducers used in high throughput screening of complementary DNA libraries.
DERWENT CLASS: B01 B02 B04 D16
INVENTOR(S): CORNISH, V W
PATENT ASSIGNEE(S): (UYCO) UNIV COLUMBIA NEW YORK; (CORN-I) CORNISH V W
COUNTRY COUNT: 100
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002059272	A2	20020801	(200267)*	EN	97
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW					
US 2002168737	A1	20021114	(200277)		
AU 2002241970	A1	20020806	(200427)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002059272	A2	WO 2002-US2199	20020124
US 2002168737	A1	US 2001-768474	20010124
AU 2002241970	A1	AU 2002-241970	20020124

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002241970	A1	Based on	WO 2002059272

PRIORITY APPLN. INFO: US 2001-768474 20010124
AN 2002-627419 [67] WPIDS
CR 2003-361751 [34]
AB WO 200259272 A UPAB: 20040429
NOVELTY - Covalent chemical inducers (I) are new.

DETAILED DESCRIPTION - Covalent chemical inducers of formula H1-Y-H2 (I) are new.

H1 = a substrate capable of selectively binding to a first receptor;

H2 = a substrate capable of selectively binding to and selectively forming a covalent bond with a second receptor, and

Y = a group forming a covalent linkage between H1 and H2, which is optionally present, and when absent, H1 is covalently linked to H2.

INDEPENDENT CLAIMS are also included for the following:

(1) a complex (a) between (I) and a fusion protein (a1) comprising a receptor domain which binds to (I);

(2) a cell comprising (a);

(3) a cell (b) comprising a DNA sequence which on transcription gives a first fusion protein (b1) exogenous to (b) and a second fusion protein (b2) exogenous to (b), where (b1) is a receptor domain fused with a **DNA-binding domain** and (b2) is a transcription **activation domain** fused to a penicillin binding protein (PBP) or to a thymidine synthase (TS) enzyme;

(4) **dimerizing** two fusion proteins inside a cell which comprises contacting (I) with a cell which expresses a first fusion protein (c1) which comprises a receptor domain that binds to H1 and a second fusion protein (c2) comprising a receptor domain that binds to and forms a covalent bond with H2;

(5) a method (A) for identifying a molecule that binds a known target in a cell from a pool of candidate molecules which comprises:

(i) forming a screening molecule by covalently bonding each molecule in the pool of candidate molecules to H2;

(ii) introducing the screening molecule into a cell culture comprising cell that express a first fusion protein of a **DNA-binding domain** fused to a known target receptor domain against which the candidate molecule is screened, a second fusion protein which comprises a receptor domain capable of binding to and forming a covalent bond with the screening molecule, and a reporter gene in which its expression is conditioned on the proximity of the first fusion protein to the second fusion protein;

(iii) permitting the screening molecule to bind to the first and the second fusion protein, bringing the two fusion proteins into proximity to activate the expression of the reporter gene;

(iv) selecting the cell that expresses the reporter gene and

(v) identifying the small molecule that binds the known target receptor;

(6) a method (A1) of identifying an unknown target receptor to which a molecule is capable of binding in the cell which comprises introducing a screening molecule having a ligand which has a specificity for the unknown target receptor covalently bonded to a substrate capable of selectively binding to and selectively forming a covalent bond with a receptor, into a cell which expresses the fusion proteins and reporter gene as in (5), (iii), permitting the screening molecule to bind to the fusion proteins to activate expression of the reporter gene, selecting which cell expresses the unknown target receptor and identifying the unknown target receptor.

(7) a new compound of formula H1a-Ya-H2a (II);

(8) a complex (d) between (II) and a fusion protein comprising a binding domain capable of binding to methotrexate and H1a binds to the binding domain of the fusion protein;

(9) a cell comprising (d);

(10) a method (A2) of screening a complementary DNA **library** by identifying the expressed protein target which comprises introducing a

screening molecule comprising the methotrexate group or its analog covalently bonded to a ligand which has a known specificity, into a cell which expresses a first fusion protein comprising a binding domain capable of binding methotrexate, a second fusion protein comprising the expressed unknown protein target and a reporter gene in which its expression is conditioned on the proximity of the first fusion protein to the second fusion protein, permitting the screening molecule to bind to the first and the second fusion protein to activate the expression of the reporter gene, selecting which cell expresses the reporter gene and identifying the unknown protein target and corresponding cDNA, and

(11) a new protein cloned by (A2).

H1a = Mtx or its analog, and

H2a = a substrate capable of binding to a receptor, and

Ya = a group providing a covalent linkage between H1a and H2a, which is optionally present and when absent, H1a is covalently linked to H2a.

ACTIVITY - None given in the source material.

MECHANISM OF ACTION - None given in the source material.

USE - Used for **dimerizing** two fusion proteins inside a cell, identifying a molecule that binds a known target in cell (e.g. insect cells, yeast cells, mammalian cell or their lysate) from a pool of candidate molecules, for identifying an unknown target receptor to which a molecule is capable of binding in a cell and for screening a cDNA **library** by identifying the expressed protein target, for screening a compound for the ability to inhibit a ligand-receptor interaction and for determining the binding specificity of a biomolecule, which is useful for understanding the mechanisms and pathways of biological system and for the future development of therapeutic and diagnostic agents.

ADVANTAGE - The compound (I) is more sensitive than the Dex-Mtx system because the covalent bond gives zero k-off for the covalent ligand-protein binding pair and then the cut-off Kd of the whole system is enhanced.

Dwg.0/24

L7 ANSWER 13 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:451388 CAPLUS

DOCUMENT NUMBER: 131:85157

TITLE: Detection of peptide modulators of protein-protein biological interactions using a transformed cellular three-hybrid system

INVENTOR(S): Watt, Paul M.; Kees, Ursula R.

PATENT ASSIGNEE(S): TVW Telethon Institute for Child Health Research, Australia

SOURCE: PCT Int. Appl., 77 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9935282	A1	19990715	WO 1999-AU18	19990108
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2317816	AA	19990715	CA 1999-2317816	19990108

AU 9922587	A1	19990726	AU 1999-22587	19990108
AU 735887	B2	20010719		
EP 1053347	A1	20001122	EP 1999-902452	19990108
R: DE, FR, GB, NL				
US 6610495	B1	20030826	US 1999-227652	19990108
PRIORITY APPLN. INFO.:			US 1998-70989P	P 19980109
			WO 1999-AU18	W 19990108

AB The present invention relates generally to a method of identifying modulators of biol. interactions and agents useful for same. More particularly, the present invention contemplates a method of detecting inhibitors of biol. interactions involving proteinaceous and/or nucleic acid mols. and more particularly a method of identifying peptide inhibitors of biol. interactions having adverse effects on living cells, tissue or organisms. A peptide **library** is produced in a cellular host wherein the transformed cells of the **library** contain (1) a nucleotide sequence encoding a reporter mol. the expression of which is operably under control of the biol. interaction and (2) a second nucleotide sequence which encodes the peptide, oligopeptide, or polypeptide placed under the control of suitable promoter. The cellular host is cultured for a time and under conditions sufficient for expression of the peptide to occur, and cells selected wherein expression of said reporter mol. is modified. The yeast/Escherichia coli shuttle vector pBLOCK-1 is constructed such that EM7 and TEF1 promoters regulate expression of the Zeocin resistance gene, while ADH1 and T7 promoters regulate expression of a nucleic acid mol. inserted into a multiple cloning site in yeast and bacteria, resp., such that the nucleic acid mol. is expressed as a fusion peptide with the SV40 nuclear localization signal and the V5 epitope. The further presence of the mammalian-expressible CMV and SV40 promoters and the SPA terminator sequence provides a mammalian/yeast/E. coli shuttle vector (pBLOCK-2). In a preferred embodiment, one polypeptide partner may comprise a **DNA-binding domain** fusion between the GAL4 DNA or LexA operator binding domain of a transcription factor and an amino acid sequence capable of **dimerization** with a second polypeptide partner, such as a region of the SCL polypeptide capable of interacting with the DRG, E47 or LMO2 proteins. A second polypeptide partner comprises an **activation domain** fusion between a transcriptional activator domain and a region of DRG, E47 or LMO2 proteins capable of interacting with the first polypeptide, and a third binding parter comprises a non-naturally occurring promoter sequence which includes the GAL4 binding site or LexA operator sequences for docking of the **DNA binding domain** fusion and other sequences as required for modulating reporter gene expression under control of the biol. interaction. Preferably, the third binding parter is operably connected to a reporter mol. comprising the URA3 structural gene which, when expressed in the presence of 5-fluororotic acid under control of the biol. interaction, will result in reduced cell growth or viability or cell death. The present invention provides the means by which a wide range of peptide-based therapeutic, prophylactic and diagnostic reagents may be developed.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 20 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 3

ACCESSION NUMBER: 1996:576593 BIOSIS
DOCUMENT NUMBER: PREV199799291274
TITLE: Interactions between Drosophila USP and ECR-A was identified in yeast two-hybrid system.
AUTHOR(S): Kim, Sa Jae [Reprint author]; Park, Ji Kweon; Ko, In Sook; Chung, Ki Wha; Lee, Chung Choo
CORPORATE SOURCE: Dep. Biol., Cheju Natl. Univ., Cheju 690-756, South Korea

SOURCE: Korean Journal of Genetics, (1996) Vol. 18, No. 3, pp. 191-198.
CODEN: KJGEDG. ISSN: 0254-5934.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Dec 1996
Last Updated on STN: 23 Dec 1996

AB Ultraspiracle gene product (USP) is one of several orphan receptors in Drosophila, sharing significant homology with the mammalian retinoid X receptor. In Drosophila the response to the hormone is mediated in part by USP and ecdysone receptors (ECR), which are members of the nuclear receptor superfamily. Heterodimers of these proteins bind to ecdysone response elements (EcRE) and ecdysone to modulate transcription. We used the yeast two-hybrid assay for detection of protein-protein interactions in vivo to screen for novel partners of USP. The GAL4 **DNA-binding domain** fused to USP was used as bait to screen a Drosophila embryonic cDNA **library** in which the cDNA was fused to the GAL4 **activation domain**. Several cDNA clones encoding proteins that interact with USP were isolated, one of which corresponded to the ecdysone receptor A isoform (ECR-A). Domain analysis on USP revealed that the ligand binding domain is required for heterodimerization with ECR-A. Given the ability of USP to **dimerize** preferentially with ECR-A, this strategy should be useful for cloning novel partners for USP from a variety of cell types.

L7 ANSWER 21 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
ACCESSION NUMBER: 1996-049675 [05] WPIDS
CROSS REFERENCE: 2002-049273 [06]
DOC. NO. CPI: C1996-016281
TITLE: Modified cells for testing cpds. for peptide binding activity - express two fusion proteins, each containing one member of a binding pair and one domain of a transcriptional activation protein, and also a reporter gene associated with this protein.
DERWENT CLASS: B04 D16
INVENTOR(S): OZENBERGER, B A; YOUNG, K H
PATENT ASSIGNEE(S): (AMCY) AMERICAN CYANAMID CO; (AMHP) WYETH HOLDINGS CORP
COUNTRY COUNT: 66
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9534646	A1	19951221	(199605)*	EN	55
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ UG					
W: AM AU BB BG BR BY CA CN CZ EE FI GE HU IS JP KG KP KR KZ LK LR LT LV MD MG MN MX NO NZ PL RO RU SG SI SK TJ TM TT UA UG UZ VN					
AU 9526066	A	19960105	(199614)		
ZA 9504892	A	19960424	(199622)		52
EP 765389	A1	19970402	(199718)	EN	
R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE					
NZ 287372	A	19971124	(199802)		
AU 706173	B	19990610	(199934)		
US 5989808	A	19991123	(200002)		
US 6251602	B1	20010626	(200138)		
US 6284519	B1	20010904	(200154)		
EP 765389	B1	20030716	(200354)	EN	
R: AT BE CH DE DK ES FR GB GR IE IT LI LT LU LV NL PT SE SI					
RU 2208646	C2	20030720	(200360)		
DE 69531302	E	20030821	(200362)		
US 6673540	B1	20040106	(200411)		
ES 2202366	T3	20040401	(200425)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9534646	A1	WO 1995-US6895	19950531
AU 9526066	A	AU 1995-26066	19950531
ZA 9504892	A	ZA 1995-4892	19950613
EP 765389	A1	EP 1995-920689	19950531
		WO 1995-US6895	19950531
NZ 287372	A	NZ 1995-287372	19950531
		WO 1995-US6895	19950531
AU 706173	B	AU 1995-26066	19950531
US 5989808	A	US 1994-259609	19940614
US 6251602	B1 Div ex	US 1994-259609	19940614
		US 1999-263944	19990308
US 6284519	B1 Cont of	US 1994-259609	19940614
		US 1999-305483	19990506
EP 765389	B1	EP 1995-920689	19950531
		WO 1995-US6895	19950531
RU 2208646	C2	WO 1995-US6895	19950531
		RU 1997-100776	19950531
DE 69531302	E	DE 1995-631302	19950531
		EP 1995-920689	19950531
		WO 1995-US6895	19950531
US 6673540	B1 Cont of	US 1994-259609	19940614
	Cont of	US 1999-305483	19990506
		US 2000-714258	20001117
ES 2202366	T3	EP 1995-920689	19950531

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9526066	A Based on	WO 9534646
EP 765389	A1 Based on	WO 9534646
NZ 287372	A Based on	WO 9534646
AU 706173	B Previous Publ.	AU 9526066
	Based on	WO 9534646
US 6251602	B1 Div ex	US 5989808
US 6284519	B1 Cont of	US 5989808
EP 765389	B1 Based on	WO 9534646
RU 2208646	C2 Based on	WO 9534646
DE 69531302	E Based on	EP 765389
	Based on	WO 9534646
US 6673540	B1 Cont of	US 5989808
	Cont of	US 6284519
ES 2202366	T3 Based on	EP 765389

PRIORITY APPLN. INFO: US 1994-259609 19940614; US
1999-263944 19990308; US
1999-305483 19990506; US
2000-714258 20001117

AN 1996-049675 [05] WPIDS

CR 2002-049273 [06]

AB WO 9534646 A UPAB: 20040810

A novel modified host cell comprising: (a) a gene sequence (I) encoding a heterologous fusion protein (II) comprising one peptide (IIa) of a binding pair (BP), or segment of it, joined to either the **DNA binding domain** or the transcriptional **activation domain** of a transcriptional activation protein (TAP); (b) gene sequence (III) encoding a heterologous fusion protein (IV) comprising a second component (IVa) of a BP, or segment of it, fused to whichever

domain of TAP is not present in (I); (c) a reporter gene (RG) operatively associated with TAP, or part of it; and (d) opt. a deletion or mutation in the host cell chromosomal DNA for the TAP, if present in the cell. The cell is able to express at least (II), (IV) and RG.

The cells are used to screen for cpds. that have peptide-binding activity, e.g. those able to affect binding of BP components, able to serve as receptor ligands or as components of multiple peptide binding complexes. Especially they are used to study ligand-dependent **dimerisation** or to identify ligand or receptor mimics, e.g. cpds. that block kinase-target, viral coat protein-cell surface receptor or Plasmodium ribonucleotide reductase subunit interactions are potentially useful as anticancer, antiviral and antimalarial agents.
Dwg.0/4

L7 ANSWER 22 OF 25 EMBASE
on STN

ACCESSION NUMBER: 94319691 EMBASE
DOCUMENT NUMBER: 1994319691
TITLE: Isolation of NF-E2-related factor 2 (Nrf2), a NF-E2-like basic leucine zipper transcriptional activator that binds to the tandem NF-E2/AP1 repeat of the β-globin locus control region.
AUTHOR: Moi P.; Chan K.; Asunis I.; Cao A.; Yuet Wai Kan
CORPORATE SOURCE: ICBEE, Universita di Cagliari,Cagliari, Italy
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1994) 91/21 (9926-9930). ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Hypersensitive site 2 located in the β-globin locus control region confers high levels of expression to the genes of the β-globin cluster. A tandem repeat of the consensus sequence for the transcription factors AP1 and NF-E2 (activating protein 1 and nuclear factor erythroid 2, respectively) is present within hypersensitive site 2 and is absolutely required for strong enhancer activity. This sequence binds, in vitro and in vivo, to ubiquitous proteins of the AP1 family and to the recently cloned erythroid-specific transcription factor NF-E2. Using the tandem repeat as a recognition site probe to screen a λgt11 cDNA expression **library** from K562 cells, we isolated several DNA binding proteins. Here, we report the characterization of one of the clones isolated. The gene, which we named Nrf2 (NF-E2-related factor 2), is encoded within a 2.2-kb transcript and predicts a 66-kDa protein with a basic leucine zipper **DNA binding domain** highly homologous to that of NF-E2. Although Nrf2 is expressed ubiquitously, a role of this protein in mediating enhancer activity of hypersensitive site 2 in erythroid cells cannot be excluded. In this respect, Nrf2 contains a powerful acidic **activation domain** that may participate in the transcriptional stimulation of β-globin genes.

L7 ANSWER 23 OF 25 MEDLINE on STN DUPLICATE 4

ACCESSION NUMBER: 93186756 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8383120
TITLE: Interactions among vertebrate helix-loop-helix proteins in yeast using the two-hybrid system.
AUTHOR: Staudinger J; Perry M; Elledge S J; Olson E N
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Texas M.D. Anderson Cancer Center, Houston 77030.

CONTRACT NUMBER: AR39849 (NIAMS)
AR40339 (NIAMS)
HD27246 (NICHD)
+
SOURCE: Journal of biological chemistry, (1993 Mar 5) 268 (7) 4608-11.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19950206
Entered Medline: 19930406

AB The helix-loop-helix (HLH) motif is contained in a rapidly growing family of transcription factors and has been shown to mediate **dimerization** among heterologous HLH-containing proteins. E12 is a widely expressed HLH protein that preferentially forms heterodimers with cell type-specific HLH proteins such as MyoD, myogenin, and the achaete-scute gene products. As a first step toward screening for novel cell type-specific partners of E12, we used a modification of the two-hybrid assay for detection of protein-protein interactions in vivo to determine whether **dimerization** of HLH proteins with E12 can occur in yeast. Using the GAL4 **DNA-binding domain** fused to the E12 HLH motif and the GAL4 transcription **activation domain** fused to MyoD, we show that E12 and MyoD can efficiently **dimerize** in yeast and reconstruct a hybrid transcription factor that activates reporter genes linked to the GAL4 DNA-binding site. The GAL4 **DNA-binding domain** fused to E12 was used to screen a mouse T-cell cDNA **library** in which the cDNA was fused to the GAL4 ***activation*** **domain**. Several cDNA clones encoding proteins that interact with E12 were isolated, one of which corresponded to the HLH protein Id-2. Given the ability of E12 to **dimerize** preferentially with cell type-specific HLH proteins, this strategy should be useful for cloning novel partners for E12 from a variety of cell types.

L7 ANSWER 24 OF 25 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 92335183 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1631061
TITLE: Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Jun.
AUTHOR: Chevray P M; Nathans D
CORPORATE SOURCE: Howard Hughes Medical Institute, Johns Hopkins University School of Medicine, Baltimore, MD 21205.
CONTRACT NUMBER: GM07309 (NIGMS)
P01 CA16519-16 (NCI)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1992 Jul 1) 89 (13) 5789-93.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M94087
ENTRY MONTH: 199208
ENTRY DATE: Entered STN: 19920904
Last Updated on STN: 19920904
Entered Medline: 19920814

AB To identify proteins that interact with Jun or Fos we have used the

protein interaction cloning system developed by S. Fields and O.-K. Song [(1989) Nature (London) 340, 245-246] to clone mammalian cDNAs encoding polypeptides that interact with the **dimerization** and DNA-binding motif (bZIP; basic domain leucine zipper motif) of Jun. For this purpose, yeast cells lacking GAL4 activity but expressing a GAL4 **DNA-binding domain**-Jun bZIP fusion protein were transformed with a mouse embryo cDNA plasmid **library** in which the cDNA was joined to a gene segment encoding the GAL4 transcriptional **activation domain.** Several transformants exhibiting GAL4 activity were identified and shown to harbor plasmids encoding polypeptides predicted to form coiled-coil structures with Jun and/or Fos. One of these is a bZIP protein of the ATF/CREB protein family--probably the murine homolog of TAXREB67. Two others encode polypeptides with predicted potential to form coiled-coil structures, and seven other isolates encode segments of alpha- or beta-tropomyosin, classical coiled-coil proteins. The tropomyosin polypeptides were found to interact in the yeast assay system with the bZIP region of Jun but not with the bZIP region of Fos. Our results illustrate the range of protein interaction cloning for discovering proteins that bind to a given target polypeptide.

L7 ANSWER 25 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

ACCESSION NUMBER: 1992:27784 BIOSIS
DOCUMENT NUMBER: PREV199293017059; BA93:17059
TITLE: THE TWO-HYBRID SYSTEM A METHOD TO IDENTIFY AND CLONE GENES FOR PROTEINS THAT INTERACT WITH A PROTEIN OF INTEREST.
AUTHOR(S): CHIEN C-T [Reprint author]; BARTEL P L; STERNGLANZ R; FIELDS S
CORPORATE SOURCE: DEP MICROBIOL, STATE UNIV NEW YORK, STONY BROOK, NY 11794, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1991) Vol. 88, No. 21, pp. 9578-9582.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 6 Jan 1992
Last Updated on STN: 6 Jan 1992

AB We describe a method that detects proteins capable of interacting with a know protein and that results in the immediate availability of the cloned genes for these interacting proteins. Plasmids are constructed to encode two hybrid proteins. One hybrid consists of the **DNA-binding domain** of the yeast transcriptional activator protein GAL4 fused to the known protein; the other hybrid consists of the GAL4 ***activation*** **domain** fused to protein sequences encoded by a **library** of yeast genomic DNA fragments. Interaction between the known protein and a protein encoded by one of the **library** plasmids leads to transcriptional activation of a reporter gene containing a binding site for GAL4. We used this method with the yeast SIR4 protein, which is involved in the transcriptional repression of yeast mating type information. (i) We used the two-hybrid system to demonstrate that SIR4 can form homodimers. (ii) A small domain consisting of the C terminus of SIR4 was shown to be sufficient to mediate this interaction. (iii) We screened a **library** to detect hybrid proteins that could interact with the SIR4 C-terminal domain and identified SIR4 from this **library.** This approach could be readily extended to mammalian proteins by the construction of appropriate cDNA libraries in the **activation domain** plasmid.

```
=> d his

     (FILE 'HOME' ENTERED AT 21:26:03 ON 07 DEC 2004)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 21:26:29 ON 07
     DEC 2004
L1         26309 DNA(W)BINDING(W)DOMAIN
L2          9597 ACTIVATION(W)DOMAIN
L3        360756 DIMER?
L4           297 L1 AND L2 AND L3
L5       2912493 TEST OR LIBRARY
L6            36 L4 AND L5
L7            25 DUP REM L6 (11 DUPLICATES REMOVED)

=> joung j/au
MISSING TERM FOR FIELD QUALIFICATION BEFORE '/AU'
The search profile entered contains a field qualifier, e.g., '/AU',
with no term preceding it.

=> e joung j/au
MISSING TERM FOR FIELD QUALIFICATION BEFORE '/AU'
The search profile entered contains a field qualifier, e.g., '/AU',
with no term preceding it.

=> e joung j/au
E1            19     JOUNG INSIL/AU
E2             1     JOUNG INSUK/AU
E3            24 --> JOUNG J/AU
E4             2     JOUNG J G/AU
E5             8     JOUNG J H/AU
E6            16     JOUNG J I/AU
E7             7     JOUNG J J/AU
E8            18     JOUNG J K/AU
E9            27     JOUNG J KEITH/AU
E10            4     JOUNG J M/AU
E11            2     JOUNG J S/AU
E12            4     JOUNG J W/AU

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L8            69 "JOUNG J"/AU OR "JOUNG J K"/AU OR "JOUNG J KEITH"/AU

=> e miller jeffrey/au
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E2             2     MILLER JEFFERY T/AU
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E4            22     MILLER JEFFREY A/AU
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E6            18     MILLER JEFFREY B/AU
E7            56     MILLER JEFFREY BOONE/AU
E8            26     MILLER JEFFREY C/AU
E9             1     MILLER JEFFREY CHRISTOPHER/AU
E10           50     MILLER JEFFREY D/AU
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E12            1     MILLER JEFFREY DOUGLAS/AU

=> e3
L9            51 "MILLER JEFFREY"/AU

=> e pabo carl/au
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E2           195     PABO C O/AU
E3             5 --> PABO CARL/AU
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E5            1     PABO CARLO O/AU
E6            2     PABO CAROL O/AU
E7            1     PABO R/AU
E8            1     PABOCHI A A/AU
E9            7     PABODIE R M/AU
E10           1     PABODIE ROBERT J/AU
E11           1     PABODIE ROBERT R/AU
E12           1     PABODLE R M/AU

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L11         454 L8 OR L9 OR L10

=> d his

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     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 21:26:29 ON 07
     DEC 2004
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L2         9597 ACTIVATION(W)DOMAIN
L3       360756 DIMER?
L4          297 L1 AND L2 AND L3
L5      2912493 TEST OR LIBRARY
L6           36 L4 AND L5
L7           25 DUP REM L6 (11 DUPLICATES REMOVED)
                E JOUNG J/AU
L8           69 E3 OR E8 OR E9
                E MILLER JEFFREY/AU
L9           51 E3
                E PABO CARL/AU
L10         352 E2-E6
L11         454 L8 OR L9 OR L10

=> l11 and l4
L12           0 L11 AND L4

=> l7 and l1
L13          25 L7 AND L1

=> l11 and l1
L14          21 L11 AND L1

=> l8 and l9 and l10
L15           2 L8 AND L9 AND L10

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PROCESSING COMPLETED FOR L15
L16           2 DUP REM L15 (0 DUPLICATES REMOVED)

=> t ti l16 1-2

L16  ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
TI   Methods and compositions for interaction trap assays
```

L16 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
TI Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions

=> dup rem l7
PROCESSING COMPLETED FOR L7
L17 25 DUP REM L7 (0 DUPLICATES REMOVED)

=> t ti l17 1-25

L17 ANSWER 1 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Novel compound comprising two portions obtained from steroids, hormones or drugs, joined by enzyme cleavable moiety such as amide or cephem moiety, useful for screening proteins capable of catalyzing bond cleavage.

L17 ANSWER 2 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Bacterial small-mol. three-hybrid system comprising **dimeric** Mtx-SLF ligand that bridges λcI and NTD fusion proteins for detecting protein-small molecule interactions

L17 ANSWER 3 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New non-single chain antigen-binding units stabilized by leucine zipper sequences, useful for diagnostic and therapeutic purposes, and as building blocks for constructing multivalent and/or multispecific antibodies.

L17 ANSWER 4 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Expression and influence of Jun factors in erythroid and megakaryocytic differentiation of primary human hematopoietic progenitors.

L17 ANSWER 5 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Synthetic derivatives of DNA-binding peptides for use in the therapeutic regulation of gene expression

L17 ANSWER 6 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Yeast three-hybrid system for in vivo drug screening and enzyme evolution using chemical inducers of **dimerization**

L17 ANSWER 7 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New covalent chemical inducers used in high throughput screening of complementary DNA libraries.

L17 ANSWER 8 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Covalent chemical inducer of protein **dimerization,** useful for **dimerizing** two fusion proteins inside a cell, comprises substrates capable of selectively binding to receptors.

L17 ANSWER 9 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Improved reverse n-hybrid screening method for peptides inhibiting protein-protein or nucleic acid-protein interaction

L17 ANSWER 10 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Inducing cell to generate detectable signal and detecting entity within cell, comprises allowing stable interaction of first reporter and second reporter by binding with the entity and generating signal.

L17 ANSWER 11 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New chemical inducer of **dimerization** useful in methods of screening.

L17 ANSWER 12 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Novel chimeric protein useful for modulating exogenous gene expression in subjects, comprises two functional protein units, each containing **dimerization** domain of steroid/thyroid hormone nuclear receptor superfamily.

L17 ANSWER 13 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Detection of peptide modulators of protein-protein biological interactions using a transformed cellular three-hybrid system

L17 ANSWER 14 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Histone deacetylase inhibitors for activating hormone-responsive genes.

L17 ANSWER 15 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI New method of screening for modulators of viral matrix protein interaction, useful for treating acute respiratory disease.

L17 ANSWER 16 OF 25 MEDLINE on STN
TI Identification of protein-protein interactions of the major sperm protein (MSP) of Caenorhabditis elegans.

L17 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN
TI Using genetic means to dissect homologous and heterologous protein-protein interactions of PKR, the interferon-induced protein kinase

L17 ANSWER 18 OF 25 MEDLINE on STN
TI hMAF, a small human transcription factor that heterodimerizes specifically with Nrf1 and Nrf2.

L17 ANSWER 19 OF 25 MEDLINE on STN
TI A novel, transformation-relevant **activation domain** in Fos proteins.

L17 ANSWER 20 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Interactions between Drosophila USP and ECR-A was identified in yeast two-hybrid system.

L17 ANSWER 21 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Modified cells for testing cpds. for peptide binding activity - express two fusion proteins, each containing one member of a binding pair and one domain of a transcriptional activation protein, and also a reporter gene associated with this protein.

L17 ANSWER 22 OF 25 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI Isolation of NF-E2-related factor 2 (Nrf2), a NF-E2-like basic leucine zipper transcriptional activator that binds to the tandem NF-E2/AP1 repeat of the β-globin locus control region.

L17 ANSWER 23 OF 25 MEDLINE on STN
TI Interactions among vertebrate helix-loop-helix proteins in yeast using the two-hybrid system.

L17 ANSWER 24 OF 25 MEDLINE on STN
TI Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Jun.

L17 ANSWER 25 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI THE TWO-HYBRID SYSTEM A METHOD TO IDENTIFY AND CLONE GENES FOR PROTEINS THAT INTERACT WITH A PROTEIN OF INTEREST.

=> d his

(FILE 'HOME' ENTERED AT 21:26:03 ON 07 DEC 2004)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 21:26:29 ON 07 DEC 2004

L1	26309	DNA(W)BINDING(W)DOMAIN
L2	9597	ACTIVATION(W)DOMAIN
L3	360756	DIMER?
L4	297	L1 AND L2 AND L3
L5	2912493	TEST OR LIBRARY
L6	36	L4 AND L5
L7	25	DUP REM L6 (11 DUPLICATES REMOVED)
		E JOUNG J/AU
L8	69	E3 OR E8 OR E9
		E MILLER JEFFREY/AU
L9	51	E3
		E PABO CARL/AU
L10	352	E2-E6
L11	454	L8 OR L9 OR L10
L12	0	L11 AND L4
L13	25	L7 AND L1
L14	21	L11 AND L1
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L16	2	DUP REM L15 (0 DUPLICATES REMOVED)
L17	25	DUP REM L7 (0 DUPLICATES REMOVED)

=> d ibib abs l17 17-25

L17 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	1998:618193 CAPLUS
DOCUMENT NUMBER:	129:327641
TITLE:	Using genetic means to dissect homologous and heterologous protein-protein interactions of PKR, the interferon-induced protein kinase
AUTHOR(S):	Tan, Seng-Lai; Katze, Michael G.
CORPORATE SOURCE:	Department of Microbiology, School of Medicine, University of Washington, Seattle, WA, 98195, USA
SOURCE:	Methods (Orlando, Florida) (1998), 15(3), 207-223 CODEN: MTHDE9; ISSN: 1046-2023
PUBLISHER:	Academic Press
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB The interferon-induced protein kinase, PKR, is a pivotal component of interferon (IFN)-induced cellular antiviral and antiproliferative response. The identification and characterization of proteins, of both viral and cellular origins, that interact with PKR have proven to be a valuable probe for unraveling the cellular regulation and function of PKR. Several studies have demonstrated that PKR forms **dimers** and that **dimerization** is likely to be required for activation and/or catalytic function. It is therefore important to elucidate the mechanism of PKR **dimer** formation and the role of PKR effectors in modulating kinase **dimerization**. Herein we describe the use of the two genetic approaches, the δ repressor fusion and the yeast two-hybrid systems, to detect and analyze homo- and heterotypic interactions with PKR. We also describe several biochem. methodologies commonly used in our laboratory to validate the genetic results. Although the examples in this article focus on PKR, the techniques can easily be adapted to investigate protein-protein assocns. in a variety of exptl. systems. Finally, given the important role of PKR as a mediator of

IFN-induced antiviral and antiproliferative effects, these studies may provide clues to the development of reagents that target PKR to enhance the therapeutic use of IFN in the treatment of disease. (c) 1998 Academic Press.

REFERENCE COUNT: 121 THERE ARE 121 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 18 OF 25 MEDLINE on STN
ACCESSION NUMBER: 97341189 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9195958
TITLE: hMAF, a small human transcription factor that heterodimerizes specifically with Nrf1 and Nrf2.
AUTHOR: Marini M G; Chan K; Casula L; Kan Y W; Cao A; Moi P
CORPORATE SOURCE: Istituto di Clinica e Biologia dell'Eta Evolutiva, Universita di Cagliari, Cagliari 09121, Italy.
CONTRACT NUMBER: DK16666 (NIDDK)
DK50267 (NIDDK)
SOURCE: Journal of biological chemistry, (1997 Jun 27) 272 (26) 16490-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y11514
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970724
Last Updated on STN: 19980206
Entered Medline: 19970716

AB A 1.6-kilobase pair full-length cDNA encoding a transcription factor homologous to the Maf family of proteins was isolated by screening a K562 cDNA **library** with the NFE2 tandem repeat probe derived from the globin locus control region. The protein, which was designated hMAF, contains a basic **DNA binding domain** and an extended leucine zipper but lacks any recognizable **activation domain**. Expressed in vitro, the hMAF protein is able to homodimerize in solution and band-shift the NFE2 tandem repeat probe. In addition to homodimers, hMAF can also form high affinity heterodimers with two members of the NFE2/CNC-bZip family (Nrf1 and Nrf2) but not with a third family member, p45-NFE2. Although hMAF/hMAF homodimers and hMAF/Nrf1 and hMAF/Nrf2 heterodimers bind to the same NFE2 site, they exert functionally opposite effects on the activity of a linked gamma-globin gene. In fact, whereas all hMAF/CNC-bZip heterodimers stimulate the activity of a gamma-promoter reporter construct in K562 cells, the association into homodimers that is induced by overexpressing hMAF inhibits the activity of the same construct. Thus variations in the expression of hMAF may account for the modulation in the activity of the genes that bear NFE2 recognition sites.

L17 ANSWER 19 OF 25 MEDLINE on STN
ACCESSION NUMBER: 97154488 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9001206
TITLE: A novel, transformation-relevant **activation domain** in Fos proteins.
AUTHOR: Funk M; Poensgen B; Graulich W; Jerome V; Muller R
CORPORATE SOURCE: Institut fur Molekularbiologie und Tumorforschung, Phillips-Universitat Marburg, Germany.
SOURCE: Molecular and cellular biology, (1997 Feb) 17 (2) 537-44.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 19970305
Last Updated on STN: 19970305
Entered Medline: 19970218

AB We have previously demonstrated that transformation by Fos is critically dependent on an intact **DNA-binding domain** (bZip) and a functional N-terminal transactivation motif (N-TM). We now show that a novel motif (C-terminal transactivation motif [C-TM]) near the C terminus also plays an important role in both transformation and the activation of AP1-dependent transcription and that the hydrophobic amino acids in the C-TM are functionally essential. The C-TM is the most crucial element in the C-terminal transactivation domain in Fos, as indicated by its relative strength and context-independent function. The C-TM is clearly different from the previously identified HOB2 domain, located N terminally to the C-TM, and the C-terminally positioned TATA-binding protein-binding domain. We also show that the C-terminal transactivation domain strongly synergizes with the HOB1-like N-TM, even when both domains are present on different proteins within a **dimeric** complex, and that the C-TM plays a crucial role in this cooperation. These observations can be corroborated in a model in which multiple contacts with the basal machinery are established either to stabilize the transcription complex or to facilitate its sequential assembly.

L17 ANSWER 20 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 1996:576593 BIOSIS
DOCUMENT NUMBER: PREV199799291274
TITLE: Interactions between Drosophila USP and ECR-A was identified in yeast two-hybrid system.
AUTHOR(S): Kim, Sa Jae [Reprint author]; Park, Ji Kweon; Ko, In Sook; Chung, Ki Wha; Lee, Chung Choo
CORPORATE SOURCE: Dep. Biol., Cheju Natl. Univ., Cheju 690-756, South Korea
SOURCE: Korean Journal of Genetics, (1996) Vol. 18, No. 3, pp. 191-198.
CODEN: KJGEDG. ISSN: 0254-5934.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Dec 1996
Last Updated on STN: 23 Dec 1996

AB Ultraspiracle gene product (USP) is one of several orphan receptors in Drosophila, sharing significant homology with the mammalian retinoid X receptor. In Drosophila the response to the hormone is mediated in part by USP and ecdysone receptors (ECR), which are members of the nuclear receptor superfamily. Heterodimers of these proteins bind to ecdysone response elements (EcRE) and ecdysone to modulate transcription. We used the yeast two-hybrid assay for detection of protein-protein interactions in vivo to screen for novel partners of USP. The GAL4 **DNA-binding domain** fused to USP was used as bait to screen a Drosophila embryonic cDNA **library** in which the cDNA was fused to the GAL4 **activation domain**. Several cDNA clones encoding proteins that interact with USP were isolated, one of which corresponded to the ecdysone receptor A isoform (ECR-A). Domain analysis on USP revealed that the ligand binding domain is required for heterodimerization with ECR-A. Given the ability of USP to **dimerize** preferentially with ECR-A, this strategy should be useful for cloning novel partners for USP from a variety of cell types.

L17 ANSWER 21 OF 25 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
ACCESSION NUMBER: 1996-049675 [05] WPIDS

CROSS REFERENCE: 2002-049273 [06]
DOC. NO. CPI: C1996-016281
TITLE: Modified cells for testing cpds. for peptide binding activity - express two fusion proteins, each containing one member of a binding pair and one domain of a transcriptional activation protein, and also a reporter gene associated with this protein.
DERWENT CLASS: B04 D16
INVENTOR(S): OZENBERGER, B A; YOUNG, K H
PATENT ASSIGNEE(S): (AMCY) AMERICAN CYANAMID CO; (AMHP) WYETH HOLDINGS CORP
COUNTRY COUNT: 66
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9534646	A1	19951221	(199605)*	EN	55
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ UG					
W: AM AU BB BG BR BY CA CN CZ EE FI GE HU IS JP KG KP KR KZ LK LR LT					
LV MD MG MN MX NO NZ PL RO RU SG SI SK TJ TM TT UA UG UZ VN					
AU 9526066	A	19960105	(199614)		
ZA 9504892	A	19960424	(199622)		52
EP 765389	A1	19970402	(199718)	EN	
R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE					
NZ 287372	A	19971124	(199802)		
AU 706173	B	19990610	(199934)		
US 5989808	A	19991123	(200002)		
US 6251602	B1	20010626	(200138)		
US 6284519	B1	20010904	(200154)		
EP 765389	B1	20030716	(200354)	EN	
R: AT BE CH DE DK ES FR GB GR IE IT LI LT LU LV NL PT SE SI					
RU 2208646	C2	20030720	(200360)		
DE 69531302	E	20030821	(200362)		
US 6673540	B1	20040106	(200411)		
ES 2202366	T3	20040401	(200425)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9534646	A1		WO 1995-US6895	19950531
AU 9526066	A		AU 1995-26066	19950531
ZA 9504892	A		ZA 1995-4892	19950613
EP 765389	A1		EP 1995-920689	19950531
			WO 1995-US6895	19950531
NZ 287372	A		NZ 1995-287372	19950531
			WO 1995-US6895	19950531
AU 706173	B		AU 1995-26066	19950531
US 5989808	A		US 1994-259609	19940614
US 6251602	B1	Div ex	US 1994-259609	19940614
			US 1999-263944	19990308
US 6284519	B1	Cont of	US 1994-259609	19940614
			US 1999-305483	19990506
EP 765389	B1		EP 1995-920689	19950531
			WO 1995-US6895	19950531
RU 2208646	C2		WO 1995-US6895	19950531
			RU 1997-100776	19950531
DE 69531302	E		DE 1995-631302	19950531
			EP 1995-920689	19950531
			WO 1995-US6895	19950531
US 6673540	B1	Cont of	US 1994-259609	19940614
		Cont of	US 1999-305483	19990506
			US 2000-714258	20001117

ES 2202366 T3 EP 1995-920689 19950531

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9526066	A	Based on	WO 9534646
EP 765389	A1	Based on	WO 9534646
NZ 287372	A	Based on	WO 9534646
AU 706173	B	Previous Publ.	AU 9526066
		Based on	WO 9534646
US 6251602	B1	Div ex	US 5989808
US 6284519	B1	Cont of	US 5989808
EP 765389	B1	Based on	WO 9534646
RU 2208646	C2	Based on	WO 9534646
DE 69531302	E	Based on	EP 765389
		Based on	WO 9534646
US 6673540	B1	Cont of	US 5989808
		Cont of	US 6284519
ES 2202366	T3	Based on	EP 765389

PRIORITY APPLN. INFO: US 1994-259609 19940614; US 1999-263944 19990308; US 1999-305483 19990506; US 2000-714258 20001117

AN 1996-049675 [05] WPIDS

CR 2002-049273 [06]

AB WO 9534646 A UPAB: 20040810

A novel modified host cell comprising: (a) a gene sequence (I) encoding a heterologous fusion protein (II) comprising one peptide (IIa) of a binding pair (BP), or segment of it, joined to either the **DNA binding domain** or the transcriptional **activation domain** of a transcriptional activation protein (TAP); (b) gene sequence (III) encoding a heterologous fusion protein (IV) comprising a second component (IVa) of a BP, or segment of it, fused to whichever domain of TAP is not present in (I); (c) a reporter gene (RG) operatively associated with TAP, or part of it; and (d) opt. a deletion or mutation in the host cell chromosomal DNA for the TAP, if present in the cell. The cell is able to express at least (II), (IV) and RG.

The cells are used to screen for cpds. that have peptide-binding activity, e.g. those able to affect binding of BP components, able to serve as receptor ligands or as components of multiple peptide binding complexes. Especially they are used to study ligand-dependent **dimerisation** or to identify ligand or receptor mimics, e.g. cpds. that block kinase-target, viral coat protein-cell surface receptor or Plasmodium ribonucleotide reductase subunit interactions are potentially useful as anticancer, antiviral and antimalarial agents.

Dwg.0/4

L17 ANSWER 22 OF 25 EMBASE on STN

ACCESSION NUMBER: 94319691 EMBASE

DOCUMENT NUMBER: 1994319691

TITLE: Isolation of NF-E2-related factor 2 (Nrf2), a NF-E2-like basic leucine zipper transcriptional activator that binds to the tandem NF-E2/AP1 repeat of the β-globin locus control region.

AUTHOR: Moi P.; Chan K.; Asunis I.; Cao A.; Yuet Wai Kan

CORPORATE SOURCE: ICBEE, Universita di Cagliari,Cagliari, Italy

SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1994) 91/21 (9926-9930). ISSN: 0027-8424 CODEN: PNASA6

COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Hypersensitive site 2 located in the β-globin locus control region confers high levels of expression to the genes of the β-globin cluster. A tandem repeat of the consensus sequence for the transcription factors AP1 and NF-E2 (activating protein 1 and nuclear factor erythroid 2, respectively) is present within hypersensitive site 2 and is absolutely required for strong enhancer activity. This sequence binds, in vitro and in vivo, to ubiquitous proteins of the AP1 family and to the recently cloned erythroid-specific transcription factor NF-E2. Using the tandem repeat as a recognition site probe to screen a λgt11 cDNA expression **library** from K562 cells, we isolated several DNA binding proteins. Here, we report the characterization of one of the clones isolated. The gene, which we named Nrf2 (NF-E2-related factor 2), is encoded within a 2.2-kb transcript and predicts a 66-kDa protein with a basic leucine zipper **DNA binding domain** highly homologous to that of NF-E2. Although Nrf2 is expressed ubiquitously, a role of this protein in mediating enhancer activity of hypersensitive site 2 in erythroid cells cannot be excluded. In this respect, Nrf2 contains a powerful acidic **activation domain** that may participate in the transcriptional stimulation of β-globin genes.

L17 ANSWER 23 OF 25 MEDLINE on STN
ACCESSION NUMBER: 93186756 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8383120
TITLE: Interactions among vertebrate helix-loop-helix proteins in yeast using the two-hybrid system.
AUTHOR: Staudinger J; Perry M; Elledge S J; Olson E N
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Texas M.D. Anderson Cancer Center, Houston 77030.
CONTRACT NUMBER: AR39849 (NIAMS)
AR40339 (NIAMS)
HD27246 (NICHD)
+
SOURCE: Journal of biological chemistry, (1993 Mar 5) 268 (7) 4608-11.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19950206
Entered Medline: 19930406

AB The helix-loop-helix (HLH) motif is contained in a rapidly growing family of transcription factors and has been shown to mediate **dimerization** among heterologous HLH-containing proteins. E12 is a widely expressed HLH protein that preferentially forms heterodimers with cell type-specific HLH proteins such as MyoD, myogenin, and the achaete-scute gene products. As a first step toward screening for novel cell type-specific partners of E12, we used a modification of the two-hybrid assay for detection of protein-protein interactions in vivo to determine whether **dimerization** of HLH proteins with E12 can occur in yeast. Using the GAL4 **DNA-binding domain** fused to the E12 HLH motif and the GAL4 transcription **activation domain** fused to MyoD, we show that E12 and

MyoD can efficiently **dimerize** in yeast and reconstruct a hybrid transcription factor that activates reporter genes linked to the GAL4 DNA-binding site. The GAL4 **DNA-binding domain** fused to E12 was used to screen a mouse T-cell cDNA **library** in which the cDNA was fused to the GAL4 ***activation*** **domain**. Several cDNA clones encoding proteins that interact with E12 were isolated, one of which corresponded to the HLH protein Id-2. Given the ability of E12 to **dimerize** preferentially with cell type-specific HLH proteins, this strategy should be useful for cloning novel partners for E12 from a variety of cell types.

L17 ANSWER 24 OF 25 MEDLINE on STN
ACCESSION NUMBER: 92335183 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1631061
TITLE: Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Jun.
AUTHOR: Chevray P M; Nathans D
CORPORATE SOURCE: Howard Hughes Medical Institute, Johns Hopkins University School of Medicine, Baltimore, MD 21205.
CONTRACT NUMBER: GM07309 (NIGMS)
P01 CA16519-16 (NCI)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1992 Jul 1) 89 (13) 5789-93. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M94087
ENTRY MONTH: 199208
ENTRY DATE: Entered STN: 19920904
Last Updated on STN: 19920904
Entered Medline: 19920814

AB To identify proteins that interact with Jun or Fos we have used the protein interaction cloning system developed by S. Fields and O.-K. Song [(1989) Nature (London) 340, 245-246] to clone mammalian cDNAs encoding polypeptides that interact with the **dimerization** and DNA-binding motif (bZIP; basic domain leucine zipper motif) of Jun. For this purpose, yeast cells lacking GAL4 activity but expressing a GAL4 **DNA-binding domain**-Jun bZIP fusion protein were transformed with a mouse embryo cDNA plasmid **library** in which the cDNA was joined to a gene segment encoding the GAL4 transcriptional **activation domain**. Several transformants exhibiting GAL4 activity were identified and shown to harbor plasmids encoding polypeptides predicted to form coiled-coil structures with Jun and/or Fos. One of these is a bZIP protein of the ATF/CREB protein family--probably the murine homolog of TAXREB67. Two others encode polypeptides with predicted potential to form coiled-coil structures, and seven other isolates encode segments of alpha- or beta-tropomyosin, classical coiled-coil proteins. The tropomyosin polypeptides were found to interact in the yeast assay system with the bZIP region of Jun but not with the bZIP region of Fos. Our results illustrate the range of protein interaction cloning for discovering proteins that bind to a given target polypeptide.

L17 ANSWER 25 OF 25 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 1992:27784 BIOSIS
DOCUMENT NUMBER: PREV199293017059; BA93:17059
TITLE: THE TWO-HYBRID SYSTEM A METHOD TO IDENTIFY AND CLONE GENES FOR PROTEINS THAT INTERACT WITH A PROTEIN OF INTEREST.

AUTHOR(S): CHIEN C-T [Reprint author]; BARTEL P L; STERNGLANZ R; FIELDS S
CORPORATE SOURCE: DEP MICROBIOL, STATE UNIV NEW YORK, STONY BROOK, NY 11794, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1991) Vol. 88, No. 21, pp. 9578-9582.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 6 Jan 1992
Last Updated on STN: 6 Jan 1992

AB We describe a method that detects proteins capable of interacting with a know protein and that results in the immediate availability of the cloned genes for these interacting proteins. Plasmids are constructed to encode two hybrid proteins. One hybrid consists of the **DNA-binding domain** of the yeast transcriptional activator protein GAL4 fused to the known protein; the other hybrid consists of the GAL4 ***activation*** **domain** fused to protein sequences encoded by a **library** of yeast genomic DNA fragments. Interaction between the known protein and a protein encoded by one of the **library** plasmids leads to transcriptional activation of a reporter gene containing a binding site for GAL4. We used this method with the yeast SIR4 protein, which is involved in the transcriptional repression of yeast mating type information. (i) We used the two-hybrid system to demonstrate that SIR4 can form homodimers. (ii) A small domain consisting of the C terminus of SIR4 was shown to be sufficient to mediate this interaction. (iii) We screened a **library** to detect hybrid proteins that could interact with the SIR4 C-terminal domain and identified SIR4 from this **library**. This approach could be readily extended to mammalian proteins by the construction of appropriate cDNA libraries in the **activation domain** plasmid.

=> d his

(FILE 'HOME' ENTERED AT 21:26:03 ON 07 DEC 2004)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 21:26:29 ON 07 DEC 2004

L1	26309	DNA(W)BINDING(W)DOMAIN
L2	9597	ACTIVATION(W)DOMAIN
L3	360756	DIMER?
L4	297	L1 AND L2 AND L3
L5	2912493	TEST OR LIBRARY
L6	36	L4 AND L5
L7	25	DUP REM L6 (11 DUPLICATES REMOVED)
		E JOUNG J/AU
L8	69	E3 OR E8 OR E9
		E MILLER JEFFREY/AU
L9	51	E3
		E PABO CARL/AU
L10	352	E2-E6
L11	454	L8 OR L9 OR L10
L12	0	L11 AND L4
L13	25	L7 AND L1
L14	21	L11 AND L1
L15	2	L8 AND L9 AND L10
L16	2	DUP REM L15 (0 DUPLICATES REMOVED)
L17	25	DUP REM L7 (0 DUPLICATES REMOVED)

=> dup rem 18
PROCESSING COMPLETED FOR L8
L18 41 DUP REM L8 (28 DUPLICATES REMOVED)

=> t ti l18 1-41

L18 ANSWER 1 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI Methods for isolating NRSF-based non-natural multi-zinc finger (Zf) proteins that bind to an extended target DNA sequence of interest

L18 ANSWER 2 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Inclined line through float for use in fishing has plate shaped detachable rudder that is fitted in a groove formed along bore of float main body such that rudder portion is exposed.

L18 ANSWER 3 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Data monitoring system for communication network, has mobile station-packet data serving node monitoring system to sense received wireless and data communication environment with global positioning system time information.

L18 ANSWER 4 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Coreless type linear motor for generating propulsive force, has unit coils, where coils of two phases laterally face each other at their side portions, in central opening of unit coil of remaining phase.

L18 ANSWER 5 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Radiation detector for use in nuclear medicine imaging system, has carbon-based photodiodes, each having p-type and n-type semiconductors creating bulk heterojunction region that creates electron and hole when photon is absorbed.

L18 ANSWER 6 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Packet classification apparatus in internet, classifies packet by field based on previous classification result to process range look-up included in result.

L18 ANSWER 7 OF 41 MEDLINE on STN DUPLICATE 1
TI Allosteric inhibition of zinc-finger binding in the major groove of DNA by minor-groove binding ligands.

L18 ANSWER 8 OF 41 MEDLINE on STN DUPLICATE 2
TI High-throughput beta-galactosidase assay for bacterial cell-based reporter systems.

L18 ANSWER 9 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI High-throughput β-galactosidase assay for bacterial cell-based reporter systems

L18 ANSWER 10 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Iron core linear motor for electronic equipment and having a liquid cooling system e.g. water.

L18 ANSWER 11 OF 41 MEDLINE on STN DUPLICATE 3
TI Highly specific zinc finger proteins obtained by directed domain shuffling and cell-based selection.

L18 ANSWER 12 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI Methods and compositions for interaction trap assays

L18 ANSWER 13 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Mold for injection molding of e.g. helical gear, has rotatable blocks with

helical gear patterns, which are rotated in same direction to remove molded gear.

L18 ANSWER 14 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Die unit for injection molding of helical gears, has pair of rotary units provided with helical gear patterns at their inner end surfaces, which are rotatably attached to dies.

L18 ANSWER 15 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Multi-layered packet processing device for universal mobile telecommunication system, processes received data packet sequentially using multiple processing according to header of data packet.

L18 ANSWER 16 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI System for measuring multiple wireless data communication protocol.

L18 ANSWER 17 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI Yeast and bacterial two-hybrid selection systems for studying protein-protein interactions

L18 ANSWER 18 OF 41 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.

L18 ANSWER 19 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
TI Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions

L18 ANSWER 20 OF 41 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI A high resolution animal PET: Using continuous LSO with intrinsic spatial resolution approaching 1 mm.

L18 ANSWER 21 OF 41 MEDLINE on STN DUPLICATE 5
TI Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.

L18 ANSWER 22 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Neck portion for ground magnetic field shield tape of color CRT, has extended portions from shield object formed from material having high magnetic permeability and low coercive force.

L18 ANSWER 23 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Cyclone dust collecting device positionable at the extension of a vacuum cleaner has two tubes connected to an extension pipe, with removable tub combined with cyclone body.

L18 ANSWER 24 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Automatic data transmission rate controlling device for prevention of generation of an overflow in Ethernet switch includes pair of ports each supporting variety of transmission rates.

L18 ANSWER 25 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Packet switching apparatus for data network, includes transmission/reception control sections for accessing information resources classified into groups and ports for taking charge of input/output of packet transmission/reception commands.

L18 ANSWER 26 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Flow control method for packet switched network uses Ethernet switch with several input ports connected to several Ethernet switches upstream

devices and common memory for storing received packet data from each input port.

L18 ANSWER 27 OF 41 MEDLINE on STN DUPLICATE 6
TI A bacterial two-hybrid selection system for studying protein-DNA and protein-protein interactions.

L18 ANSWER 28 OF 41 MEDLINE on STN DUPLICATE 7
TI Blocking catabolism with eniluracil enhances PET studies of 5-[18F]fluorouracil pharmacokinetics.

L18 ANSWER 29 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI Interaction trap assay and its reagents

L18 ANSWER 30 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Combination type magnet assembly for color cathode ray tube - has compensation piece with compensation ring polarized on odd-number pole, for increasing amount of variation of electron beam of combined magnet rings by adjoining 2 electron beams among 3 electron beams.

L18 ANSWER 31 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Convergence compensating device for color Braun tube - has auxiliary magnet ring which contacts to neck of color Braun tube, and is polarized to at least four poles.

L18 ANSWER 32 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8
TI An interaction trap assay system using the λ repressor for use in a bacterial host

L18 ANSWER 33 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Input protection circuit for liquid crystal display - has N-type MOS transistor activated when damaging surge is at input terminal to aid voltage surge dissipation.

L18 ANSWER 34 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Liquid crystal projection system NoAbstract.

L18 ANSWER 35 OF 41 MEDLINE on STN DUPLICATE 9
TI Activation of prokaryotic transcription through arbitrary protein-protein contacts.

L18 ANSWER 36 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
TI Synergistic activation of transcription in E. coli

L18 ANSWER 37 OF 41 MEDLINE on STN DUPLICATE 10
TI Genetic strategy for analyzing specificity of dimer formation: Escherichia coli cyclic AMP receptor protein mutant altered in its dimerization specificity.

L18 ANSWER 38 OF 41 MEDLINE on STN DUPLICATE 11
TI Synergistic activation of transcription by bacteriophage lambda cI protein and E. coli cAMP receptor protein.

L18 ANSWER 39 OF 41 MEDLINE on STN DUPLICATE 12
TI Synergistic activation of transcription by Escherichia coli cAMP receptor protein.

L18 ANSWER 40 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Coating catheters of natural or synthetic rubber - using fluorinated alkoxy phospho nitrile polymer crosslinked with peroxide and alkyl aluminium cpd..

L18 ANSWER 41 OF 41 WPIDS COPYRIGHT 2004 THE THOMSON CORP on STN
TI Crosslinking fluorinated alkoxy phospho nitrile polymers - using peroxide and alkyl aluminium cpd. pref. tri iso butyl aluminium.

=> d ibib abs l18 1,8,11,17,18,19,21,27,29,32,35-39

L18 ANSWER 1 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:996299 CAPLUS
TITLE: Methods for isolating NRSF-based non-natural multi-zinc finger (Zf) proteins that bind to an extended target DNA sequence of interest
INVENTOR(S): **Joung, J. Keith**
PATENT ASSIGNEE(S): The General Hospital Corporation, USA
SOURCE: PCT Int. Appl., 140 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004099367	A2	20041118	WO 2003-US34028	20031023

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:		
US 2002-420458P	P	20021023
US 2003-466712P	P	20030430
US 2003-466889P	P	20030430
US 2003-477314P	P	20030609

AB The present invention relates to non-naturally occurring Zinc finger (Zf) proteins that are selected for binding to a DNA sequence of interest. The non-naturally occurring zinc finger proteins of the present invention are based on the sequence of zinc finger proteins having more than three zinc fingers, such as NRSF (neuron-restrictive silencing factor)/REST, and are capable of binding extended DNA target sequences with high affinity and specificity. NRSF binds to a 21 bp DNA sequence called the Neuron Restrictive Silencer Element (NRSE). The present invention provides a method for rapidly selecting multi-finger Zf polypeptides that bind to any desired sequence of interest comprising a target site, termed "context sensitive parallel optimization" (CSPO). The binding of NRSF to DNA was studied by bacterial two-hybrid system. Targeted re-engineering of NRSF zinc finger variants with altered DNA-binding specificity was demonstrated.

L18 ANSWER 8 OF 41 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2004145516 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15038156
TITLE: High-throughput beta-galactosidase assay for bacterial cell-based reporter systems.
AUTHOR: Thibodeau Stacey A; Fang Rui; **Joung J Keith**
CORPORATE SOURCE: Massachusetts General Hospital, Charlestown, MA, USA.
CONTRACT NUMBER: K08DK02883 (NIDDK)
SOURCE: BioTechniques, (2004 Mar) 36 (3) 410-5.

Journal code: 8306785. ISSN: 0736-6205.
PUB. COUNTRY: United States
DOCUMENT TYPE: (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 20040325
Last Updated on STN: 20041006
Entered Medline: 20041005

L18 ANSWER 11 OF 41 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2003481808 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14527993
TITLE: Highly specific zinc finger proteins obtained by directed domain shuffling and cell-based selection.
AUTHOR: Hurt Jessica A; Thibodeau Stacey A; Hirsh Andrew S; Pabo Carl O; **Joung J Keith**
CORPORATE SOURCE: Molecular Pathology Unit, Division of Molecular Pathology and Research, Department of Pathology, Massachusetts General Hospital, Charlestown, MA 02129, USA.
CONTRACT NUMBER: 5T32 CA 09216 (NCI)
K08 DK 02883 (NIDDK)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2003 Oct 14) 100 (21) 12271-6.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200312
ENTRY DATE: Entered STN: 20031016
Last Updated on STN: 20031219
Entered Medline: 20031204

AB Engineered Cys2His2 zinc finger proteins (ZFPs) can mediate regulation of endogenous gene expression in mammalian cells. Ideally, all zinc fingers in an engineered multifinger protein should be optimized concurrently because cooperative and context-dependent contacts can affect DNA recognition. However, the simultaneous selection of key contacts in even three fingers from fully randomized libraries would require the consideration of >10(24) possible combinations. To address this challenge, we have developed a novel strategy that utilizes directed domain shuffling and rapid cell-based selections. Unlike previously described methods, our strategy is amenable to scale-up and does not sacrifice combinatorial diversity. Using this approach, we have successfully isolated multifinger proteins with improved in vitro and in vivo function. Our results demonstrate that both DNA binding affinity and specificity are important for cellular function and also provide a general approach for optimizing multidomain proteins.

L18 ANSWER 17 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:75438 CAPLUS
DOCUMENT NUMBER: 137:226954
TITLE: Yeast and bacterial two-hybrid selection systems for studying protein-protein interactions
AUTHOR(S): Serebriiskii, Ilya; **Joung, J. Keith**
CORPORATE SOURCE: Fox Chase Cancer Center, Philadelphia, PA, 10111, USA
SOURCE: Protein-Protein Interactions (2002), 93-142.
Editor(s): Golemis, Erica. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, N. Y.
CODEN: 69CFYI; ISBN: 0-87969-628-1

DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review describes the yeast and bacterial two-hybrid systems as powerful methods for analyzing protein-protein interactions. The screening for novel proteins using the interaction trap variant of the yeast two-hybrid system is discussed. The bacterial two-hybrid system is based on the observation that two interacting proteins X and Y can trigger transcriptional activation of a weak promoter in Escherichia coli.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 18 OF 41 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2002060487 EMBASE
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.
AUTHOR: **Joung J.K.**
CORPORATE SOURCE: J.K. Joung, Department of Pathology, Division of Molecular Pathology, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129, United States. jjoung@partners.org
SOURCE: Journal of Cellular Biochemistry, (2002) 84/SUPPL. 37 (53-57).
Refs: 12
ISSN: 0730-2312 CODEN: JCEBD5
COUNTRY: United States
DOCUMENT TYPE: Journal; Conference Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A bacterial two-hybrid system based on transcriptional activation in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries > 10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying, modifying, or optimizing protein-DNA and protein-protein interactions. .COPYRGT. 2002 Wiley-Liss, Inc.

L18 ANSWER 19 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2001:851433 CAPLUS
DOCUMENT NUMBER: 136:1569
TITLE: Interaction trap assays using selectable markers to screen large libraries for protein-protein and protein-nucleic acid interactions
INVENTOR(S): **Joung, J. Keith**; Miller, Jeffrey; Pabo, Carl O.
PATENT ASSIGNEE(S): Massachusetts Institute of Technology, USA
SOURCE: PCT Int. Appl., 196 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088197	A2	20011122	WO 2001-US15718	20010516
WO 2001088197	A3	20031231		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,

GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-204509P P 20000516

AB The present invention provides methods and compns. for interaction trap assays for detecting protein-protein, protein-DNA, or protein-RNA interactions using prokaryotic or microbial eukaryotic hosts. The methods and compns. of the invention may also be used to identify agents which may agonize or antagonize a protein-protein, protein-DNA, or protein-RNA interaction. In certain embodiments, the interaction trap system of the invention is useful for screening libraries with greater than 107 members. In other embodiments, the interaction trap system of the invention is used in conjunction with flow cytometry. The invention further provides a means for simultaneously screening a target protein or nucleic acid sequence for the ability to interact with two or more test proteins or nucleic acids. In one form, the screening involves the use of a selectable marker allowing screening of large nos. of cells without the need to scan for a colorimetric marker. In a second form, screening of a colorimetric marker is by flow cytometry. Screening of a library of 108 members in Escherichia coli for C2H2 zinc finger variants is demonstrated.

L18 ANSWER 21 OF 41 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 2002121249 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11842428
TITLE: Identifying and modifying protein-DNA and protein-protein interactions using a bacterial two-hybrid selection system.
AUTHOR: **Joung J K**
CORPORATE SOURCE: Department of Pathology, Division of Molecular Pathology and Research, Massachusetts General Hospital, Charlestown, Massachusetts 02129, USA.. jjoung@partners.org
CONTRACT NUMBER: 1 K08 DK02883-01 (NIDDK)
SOURCE: Journal of cellular biochemistry. Supplement, (2001) Suppl 37 53-7. Ref: 12
Journal code: 8207539. ISSN: 0733-1959.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020222
Last Updated on STN: 20030214
Entered Medline: 20020429

AB A bacterial two-hybrid system based on transcriptional activation in E. coli has recently been described. A variety of different protein-DNA and protein-protein interactions from bacteria, yeast, and humans have been studied using this bacterial-based system. The method, because it is based in bacteria, offers significant advantages relative to its yeast counterpart including the ability to analyze complex libraries > 10(8) in size, ease of use, and speed. The ability to easily and rapidly process very large libraries make this system a powerful tool for identifying, modifying, or optimizing protein-DNA and protein-protein interactions.

L18 ANSWER 27 OF 41 MEDLINE on STN DUPLICATE 6

ACCESSION NUMBER: 2000319035 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10852947
TITLE: A bacterial two-hybrid selection system for studying protein-DNA and protein-protein interactions.
AUTHOR: **Joung J K**; Ramm E I; Pabo C O
CORPORATE SOURCE: Howard Hughes Medical Institute and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2000 Jun 20) 97 (13) 7382-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000811
Last Updated on STN: 20000811
Entered Medline: 20000731

AB We have developed a bacterial "two-hybrid" system that readily allows selection from libraries larger than 10(8) in size. Our bacterial system may be used to study either protein-DNA or protein-protein interactions, and it offers a number of potentially significant advantages over existing yeast-based one-hybrid and two-hybrid methods. We tested our system by selecting zinc finger variants (from a large randomized library) that bind tightly and specifically to desired DNA target sites. Our method allows sequence-specific zinc fingers to be isolated in a single selection step, and thus it should be more rapid than phage display strategies that typically require multiple enrichment/amplification cycles. Given the large library sizes our bacterial-based selection system can handle, this method should provide a powerful tool for identifying and optimizing protein-DNA and protein-protein interactions.

L18 ANSWER 29 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:450862 CAPLUS
DOCUMENT NUMBER: 131:83957
TITLE: Interaction trap assay and its reagents
INVENTOR(S): Dove, Simon; **Joung, J. Keith**; Hochschild, Ann
PATENT ASSIGNEE(S): President & Fellows of Harvard College, USA
SOURCE: U.S., 28 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 5925523	A	19990720	US 1997-920015		19970826
US 6200759	B1	20010313	US 1999-296204		19990421
PRIORITY APPLN. INFO.:			US 1996-24484P	P	19960823
			US 1997-918612	B2	19970822
			US 1997-920015	A1	19970826

AB The present invention makes available an interaction trap system which is derived using recombinantly engineered prokaryotic cells. An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is generally similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using fusion proteins of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a fusion protein of the α or ω subunits

of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 32 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8

ACCESSION NUMBER: 1998:151232 CAPLUS
DOCUMENT NUMBER: 128:201791
TITLE: An interaction trap assay system using the λ repressor for use in a bacterial host
INVENTOR(S): Dove, Simon; **Joung, J. Keith**; Hochschild, Ann
PATENT ASSIGNEE(S): President and Fellows of Harvard College, USA
SOURCE: PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9807845	A1	19980226	WO 1997-US14860	19970822
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9741596	A1	19980306	AU 1997-41596	19970822
PRIORITY APPLN. INFO.:			US 1996-24484P	P 19960823
			WO 1997-US14860	W 19970822

AB An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is generally similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using fusion proteins of the λ cI repressor that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a fusion protein of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 35 OF 41 MEDLINE on STN DUPLICATE 9

ACCESSION NUMBER: 97256540 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9121589
TITLE: Activation of prokaryotic transcription through arbitrary protein-protein contacts.
AUTHOR: Dove S L; **Joung J K**; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA.
SOURCE: Nature, (1997 Apr 10) 386 (6625) 627-30.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970506

Last Updated on STN: 19980206
Entered Medline: 19970422

AB Many transcriptional activators in prokaryotes are known to bind near a promoter and contact RNA polymerase, but it is not clear whether a protein-protein contact between an activator and RNA polymerase is enough to activate gene transcription. Here we show that contact between a DNA-bound protein and a heterologous protein domain fused to RNA polymerase can elicit transcriptional activation; moreover, the strength of this engineered protein-protein interaction determines the amount of gene activation. Our results indicate that an arbitrary interaction between a DNA-bound protein and RNA polymerase can activate transcription. We also find that when the DNA-bound 'activator' makes contact with two different components of the polymerase, the effect of these two interactions on transcription is synergistic.

L18 ANSWER 36 OF 41 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:634127 CAPLUS
DOCUMENT NUMBER: 127:315154
TITLE: Synergistic activation of transcription in E. coli
AUTHOR(S): Hochschild, A.; **Joung, J. K.**
CORPORATE SOURCE: Dep. Microbiology & Molecular Genetics, Harvard Medical School, Boston, MA, 02115, USA
SOURCE: Nucleic Acids and Molecular Biology (1997), 11(Mechanisms of Transcription), 101-114
CODEN: NAMBE8; ISSN: 0933-1891
PUBLISHER: Springer
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with several refs. Transcriptional activation in prokaryotes can involve the action of a single DNA-bound regulator or the combined action of two or more regulators working synergistically. In this chapter, the authors review some recent examples of transcriptional activator synergy and discuss the underlying mechanisms. For the purposes of this discussion, the authors follow the convention generally observed in the field and define transcriptional activator synergy as follows: the action of two (or more) activators is defined as synergistic if the amount of transcription observed in the presence of both activators (or both binding sites) is greater than the sum of the amts. observed with each activator acting on its own.

REFERENCE COUNT: 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 37 OF 41 MEDLINE on STN DUPLICATE 10
ACCESSION NUMBER: 96101597 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7498794
TITLE: Genetic strategy for analyzing specificity of dimer formation: Escherichia coli cyclic AMP receptor protein mutant altered in its dimerization specificity.
AUTHOR: **Joung J K**; Chung E H; King G; Yu C; Hirsh A S; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA.
SOURCE: Genes & development, (1995 Dec 1) 9 (23) 2986-96.
Journal code: 8711660. ISSN: 0890-9369.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960217
Last Updated on STN: 19960217
Entered Medline: 19960118

AB Many transcriptional regulators function in homo- or heterodimeric combinations. The same protein can carry out distinct regulatory functions depending on the partner with which it associates. Here, we describe a mutant of the Escherichia coli cAMP receptor protein (CRP) that has an altered dimerization specificity; that is, mutant/mutant homodimers form preferentially over wild-type/mutant heterodimers. CRP dimerization involves the formation of a parallel coiled-coil structure, and our CRP mutant bears an amino acid substitution affecting the first "d" position residue within the alpha-helix that mediates CRP dimerization. The genetic strategy we used to isolate this CRP altered dimerization specificity (ADS) mutant is generalizable and could be utilized to isolate ADS mutants of other dimeric transcriptional regulators.

L18 ANSWER 38 OF 41 MEDLINE on STN DUPLICATE 11
ACCESSION NUMBER: 94377980 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8091212
TITLE: Synergistic activation of transcription by bacteriophage lambda cI protein and E. coli cAMP receptor protein.
AUTHOR: **Joung J K**; Koepp D M; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA 02115.
CONTRACT NUMBER: GM44025 (NIGMS)
SOURCE: Science, (1994 Sep 23) 265 (5180) 1863-6.
Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199410
ENTRY DATE: Entered STN: 19941031
Last Updated on STN: 19980206
Entered Medline: 19941019

AB Two heterologous prokaryotic activators, the bacteriophage lambda cI protein (lambda cI) and the Escherichia coli cyclic AMP receptor protein (CRP), were shown to activate transcription synergistically from an artificial promoter bearing binding sites for both proteins. The synergy depends on a functional activation (positive control) surface on each activator. These results imply that both proteins interact directly with RNA polymerase and thus suggest a precise mechanism for transcriptional synergy: the interaction of two activators with two distinct surfaces of RNA polymerase.

L18 ANSWER 39 OF 41 MEDLINE on STN DUPLICATE 12
ACCESSION NUMBER: 93219429 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7681995
TITLE: Synergistic activation of transcription by Escherichia coli cAMP receptor protein.
AUTHOR: **Joung J K**; Le L U; Hochschild A
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA 02115.
CONTRACT NUMBER: GM44025 (NIGMS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1993 Apr 1) 90 (7) 3083-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199305
ENTRY DATE: Entered STN: 19930521
Last Updated on STN: 19980206
Entered Medline: 19930504

AB Activation of gene expression in eukaryotes generally involves the action of multiple transcription factors that function synergistically when bound near a particular target gene. Such effects have been suggested to occur because multiple activators can interact simultaneously with one or more components of the basal transcription machinery. In prokaryotes, examples of synergistic effects on transcription are much more limited and can often be explained by cooperative DNA binding. Here we show that the Escherichia coli cAMP receptor protein (CRP) functions synergistically to activate transcription from a derivative of the lac promoter that bears a second CRP-binding site upstream of the natural binding site. We present evidence indicating that cooperative DNA binding of two CRP dimers does not account for the magnitude of the observed cooperative activation. We suggest, instead, that the two dimers stimulate transcription directly by contacting two distinct surfaces of RNA polymerase simultaneously. Thus, synergistic activation by CRP may provide a relatively simple model for examining the molecular basis of such effects in higher organisms.

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FILE 'STNGUIDE' TEMPORARILY UNAVAILABLE
SESSION CONTINUES IN FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS'
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Enter "HELP STN" for information on contacting the nearest STN Help Desk by telephone or via SEND in the STNMAIL file.

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(FILE 'HOME' ENTERED AT 21:26:03 ON 07 DEC 2004)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 21:26:29 ON 07 DEC 2004

L1	26309	DNA(W)BINDING(W)DOMAIN
L2	9597	ACTIVATION(W)DOMAIN
L3	360756	DIMER?
L4	297	L1 AND L2 AND L3
L5	2912493	TEST OR LIBRARY
L6	36	L4 AND L5
L7	25	DUP REM L6 (11 DUPLICATES REMOVED)
		E JOUNG J/AU
L8	69	E3 OR E8 OR E9
		E MILLER JEFFREY/AU
L9	51	E3
		E PABO CARL/AU
L10	352	E2-E6
L11	454	L8 OR L9 OR L10
L12	0	L11 AND L4
L13	25	L7 AND L1
L14	21	L11 AND L1
L15	2	L8 AND L9 AND L10
L16	2	DUP REM L15 (0 DUPLICATES REMOVED)
L17	25	DUP REM L7 (0 DUPLICATES REMOVED)
L18	41	DUP REM L8 (28 DUPLICATES REMOVED)

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FULL ESTIMATED COST	169.93	170.14

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-7.00	-7.00

STN INTERNATIONAL LOGOFF AT 22:00:02 ON 07 DEC 2004